

SEQUENCE LISTING

<110> Saris, Chris

<120> ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TMST2, A NOVEL
MEMBER OF THE TNF-RECEPTOR SUPERFAMILY OF GENES

<130> 01017/35434B

<140> To be assigned

<141> Herewith

<150> US 09/612,033

<151> 2000-07-07

<150> US 60/143,063

<151> 1999-07-09

<160> 15

<170> PatentIn Ver. 2.0

<210> 1

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<220>

<221> misc_feature

<222> (25)..(33)

<223> N = A or T or G or C

<220>

<223> Primer 1360-38

<400> 1

ggaaggaaaa aagcggccgc aacannnnnn nnn 33

<210> 2

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<220>

<223> Primer 1605-21

<400> 2

aatccgatgc ccacgttgca gta 23

<210> 3

<211> 26

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<220>
<223> Primer 1239-08

<400> 3
aaaatccttag accgacgact gtgttt 26

<210> 4
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<220>
<223> Primer 1605-22

<400> 4
gagtctccgc agccttttga gg 22

<210> 5
<211> 412
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (13)..(411)

<220>
<223> tmst2 00004-d1

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Met Phe Gly Phe Phe Cys Ser Leu Val Ser Ser Leu Ser
1 5 10

cgc tgg ttc ctt tgg cgg cgg ctg ctg ctg ctg ctg ctg ctg ctg ctg 99
Arg Trp Phe Leu Trp Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu
15 20 25

ctg aat ctg ccc ttg cag gta aaa ttt gct atg cta gaa tta cac tcc 147
Leu Asn Leu Pro Leu Gln Val Lys Phe Ala Met Leu Glu Leu His Ser
30 35 40 45

ttc aaa tgt ccc gct ggt gaa tac tgg tct aaa gac gtc tgt tgc aag 195
Phe Lys Cys Pro Ala Gly Glu Tyr Trp Ser Lys Asp Val Cys Cys Lys
50 55 60

aac tgt tct gca ggt aca ttt gtc aag gcg ccc tgc gaa atc ccc cat 243
Asn Cys Ser Ala Gly Thr Phe Val Lys Ala Pro Cys Glu Ile Pro His
65 70 75

act caa gga caa tgt gag aag tgt cac cca gga aca ttc aca gag aaa 291
Thr Gln Gly Gln Cys Glu Lys Cys His Pro Gly Thr Phe Thr Glu Lys
80 85 90

gat aat tac ctg gat gct tgt ata ctt tgc tcc acc tgt gat aaa gat 339
 Asp Asn Tyr Leu Asp Ala Cys Ile Leu Cys Ser Thr Cys Asp Lys Asp
 95 100 105

cag gaa atg gtg gcc gac tgc tca gcc acc agt gac cgg aaa tgc cag 387
 Gln Glu Met Val Ala Asp Cys Ser Ala Thr Ser Asp Arg Lys Cys Gln
 110 115 120 125

tgc cga aca ggt ctt tac tac tat g 412
 Cys Arg Thr Gly Leu Tyr Tyr Tyr
 130

<210> 6
 <211> 133
 <212> PRT
 <213> Mus musculus

<400> 6.
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 1 5 10 15

Leu Trp Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Asn Leu
 20 25 30

Pro Leu Gln Val Lys Phe Ala Met Leu Glu Leu His Ser Phe Lys Cys
 35 40 45

Pro Ala Gly Glu Tyr Trp Ser Lys Asp Val Cys Cys Lys Asn Cys Ser
 50 55 60

Ala Gly Thr Phe Val Lys Ala Pro Cys Glu Ile Pro His Thr Gln Gly
 65 70 75 80

Gln Cys Glu Lys Cys His Pro Gly Thr Phe Thr Glu Lys Asp Asn Tyr
 85 90 95

Leu Asp Ala Cys Ile Leu Cys Ser Thr Cys Asp Lys Asp Gln Glu Met
 100 105 110

Val Ala Asp Cys Ser Ala Thr Ser Asp Arg Lys Cys Gln Cys Arg Thr
 115 120 125

Gly Leu Tyr Tyr Tyr
 130

<210> 7
 <211> 1550
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (13)..(606)

<220>
 <223> mouse tmst2

<400> 7
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 Met Phe Gly Phe Phe Cys Ser Leu Val Ser Ser Leu Ser
 1 5 10

cgc tgg ttc ctt tgg cgg cgg ctg ctg ctg ctg ctg ctg ctg ctg ctg	99
Arg Trp Phe Leu Trp Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu	
15 20 25	
ctg aat ctg ccc ttg cag gta aaa ttt gct atg cta gaa tta cac tcc	147
Leu Asn Leu Pro Leu Gln Val Lys Phe Ala Met Leu Glu Leu His Ser	
30 35 40 45	
ttc aaa tgt ccc gct ggt gaa tac tgg tct aaa gac gtc tgt tgc aag	195
Phe Lys Cys Pro Ala Gly Glu Tyr Trp Ser Lys Asp Val Cys Cys Lys	
50 55 60	
aac tgt tct gca ggt aca ttt gtc aag gcg ccc tgc gaa atc ccc cat	243
Asn Cys Ser Ala Gly Thr Phe Val Lys Ala Pro Cys Glu Ile Pro His	
65 70 75	
act caa gga caa tgt gag aag tgt cac cca gga aca ttc aca gag aaa	291
Thr Gln Gly Gln Cys Glu Lys Cys His Pro Gly Thr Phe Thr Glu Lys	
80 85 90	
gat aat tac ctg gat gct tgt ata ctt tgc tcc acc tgt gat aaa gat	339
Asp Asn Tyr Leu Asp Ala Cys Ile Leu Cys Ser Thr Cys Asp Lys Asp	
95 100 105	
cag gaa atg gtg gcc gac tgc tca gcc acc agt gac cgg aaa tgc cag	387
Gln Glu Met Val Ala Asp Cys Ser Ala Thr Ser Asp Arg Lys Cys Gln	
110 115 120 125	
tgc cga aca ggt ctt tac tac tat gac cca aaa ttt cca gaa tgc tgc	435
Cys Arg Thr Gly Leu Tyr Tyr Tyr Asp Pro Lys Phe Pro Glu Ser Cys	
130 135 140	
cgc cca tgt acc aag tgt ccc caa gga atc cct gtc ctc cag gaa tgc	483
Arg Pro Cys Thr Lys Cys Pro Gln Gly Ile Pro Val Leu Gln Glu Cys	
145 150 155	
aac tcc aca gct aac act gtg tgc agt tca tct gtt tca aat ccc aga	531
Asn Ser Thr Ala Asn Thr Val Cys Ser Ser Ser Val Ser Asn Pro Arg	
160 165 170	
aac cgg ctg ttc cta ctg tta tca cct ttg agt gtg cta att gtg tcc	579
Asn Arg Leu Phe Leu Leu Leu Ser Pro Leu Ser Val Leu Ile Val Ser	
175 180 185	
gtt gtt gtc ttc cgt atc ata aga aga taaaggttct acagatgttt	626
Val Val Val Phe Arg Ile Ile Arg Arg	
190 195	
tcttagcttc cttttattgc tatgaagtga tactatggag gcaactcttt tattttattt	686
attttatttt attttttaat gtcttgaact tgatttgaag accaggctgg cctcaaaatc	746
acagagatcc agactaagac aactctaata agggaaacat ttaattggga ctggcattaca	806
gtttcggacg ttttgtccat gattatcata gtgggaagca tggcagcatc taagcagaca	866
tgatgttgga gaaggagctg agatttctgc atcttgatct gcaagcaata aaaggagact	926
gtgtgccaca ctatacacag cttgaacata ggagacctca aagcctgtcc ccacagtgc	986
aaacttcttc caacaaggtc atacctccta ataataccat ttcttatgag gcaagcattc	1046
aaacacatga gtctatgagg gccaaaccaa ttcaaaccac cacagggttaa caattgcct	1106

ctgcagctct ctggtggagg cctccttga gagtaagtaa caatttagat gaaggcaagt 1166
cctggtatca ggtccaaaag aaactcagga tgaatgggtcc actgtgggttc ctattaacat 1226
actgaagaac atgacctcac cttacacgtc tccacctcac tgacttccct tcccctagct 1286
tctcattccc aggtaaccct gccatTTTTT ggtaatgtgc cttcttggtt cttcctctcc 1346
tttccccctc tcttctgggtc cttacttctc ttctctccc actctccacc agcctcctct 1406
taaggcctga atcagtctgt aggtcatggt taatctacta ctttctctct gctctggact 1466
catccagatg tctctggctg agctctccct cctatctaca ataaaaacct tccccctaac 1526
cagaaatgca aaaaaaaaaa aaaa 1550

<210> 8
<211> 198
<212> PRT
<213> Mus musculus

<400> 8
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Leu Trp Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Asn Leu
20 25 30
Pro Leu Gln Val Lys Phe Ala Met Leu Glu Leu His Ser Phe Lys Cys
35 40 45
Pro Ala Gly Glu Tyr Trp Ser Lys Asp Val Cys Cys Lys Asn Cys Ser
50 55 60
Ala Gly Thr Phe Val Lys Ala Pro Cys Glu Ile Pro His Thr Gln Gly
65 70 75 80
Gln Cys Glu Lys Cys His Pro Gly Thr Phe Thr Glu Lys Asp Asn Tyr
85 90 95
Leu Asp Ala Cys Ile Leu Cys Ser Thr Cys Asp Lys Asp Gln Glu Met
100 105 110
Val Ala Asp Cys Ser Ala Thr Ser Asp Arg Lys Cys Gln Cys Arg Thr
115 120 125
Gly Leu Tyr Tyr Tyr Asp Pro Lys Phe Pro Glu Ser Cys Arg Pro Cys
130 135 140
Thr Lys Cys Pro Gln Gly Ile Pro Val Leu Gln Glu Cys Asn Ser Thr
145 150 155 160
Ala Asn Thr Val Cys Ser Ser Ser Val Ser Asn Pro Arg Asn Arg Leu
165 170 175
Phe Leu Leu Leu Ser Pro Leu Ser Val Leu Ile Val Ser Val Val Val
180 185 190
Phe Arg Ile Ile Arg Arg
195

<210> 9
<211> 702
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (13)..(552)

<220>
<223> Primer 2086-39

<400> 9
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1 5 10
cgc tgg ttc ctt tgg cgg cgg ctg ctg ctg ctg ctg ctg ctg ctg ctg 99
Arg Trp Phe Leu Trp Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu
15 20 25
ctg aat ctg ccc ttg cag gta aaa ttt gct atg cta gaa tta cac tcc 147
Leu Asn Leu Pro Leu Gln Val Lys Phe Ala Met Leu Glu Leu His Ser
30 35 40 45
ttc aaa tgt ccc gct ggt gaa tac tgg tct aaa gac gtc tgt tgc aag 195
Phe Lys Cys Pro Ala Gly Glu Tyr Trp Ser Lys Asp Val Cys Cys Lys
50 55 60
aac tgt tct gca ggt aca ttt gtc aag gcg ccc tgc gaa atc ccc cat 243
Asn Cys Ser Ala Gly Thr Phe Val Lys Ala Pro Cys Glu Ile Pro His
65 70 75
act caa gga caa tgt gag aag tgt cac cca gga aca ttc aca gag aaa 291
Thr Gln Gly Gln Cys Glu Lys Cys His Pro Gly Thr Phe Thr Glu Lys
80 85 90
gat aat tac ctg gat gct tgt ata ctt tgc tcc acc tgt gat aaa gat 339
Asp Asn Tyr Leu Asp Ala Cys Ile Leu Cys Ser Thr Cys Asp Lys Asp
95 100 105
cag gaa atg gtg gcc gac tgc tca gcc acc agt gac cgg aaa tgc cag 387
Gln Glu Met Val Ala Asp Cys Ser Ala Thr Ser Asp Arg Lys Cys Gln
110 115 120 125
tgc cga aca ggt ctt tac tac tat gac cca aaa ttt cca gaa tcg tgc 435
Cys Arg Thr Gly Leu Tyr Tyr Tyr Asp Pro Lys Phe Pro Glu Ser Cys
130 135 140
cgc cca tgt acc aag tgt ccc caa gga atc cct gtc ctc cag gaa tgc 483
Arg Pro Cys Thr Lys Cys Pro Gln Gly Ile Pro Val Leu Gln Glu Cys
145 150 155
aac tcc aca gct aac act gtg tgc agt tca tct gtt tca aga aga tct 531
Asn Ser Thr Ala Asn Thr Val Cys Ser Ser Ser Val Ser Arg Arg Ser
160 165 170
gcc tca gtg gcc tgg cct atc tgaatgggttc acagagatcc cagaaaccgg 582
Ala Ser Val Ala Trp Pro Ile
175 180

ctgttcctac tgttatcacc tttagagtgtg ctaattgtgt ccggttggtgt cttccgtaac 642
ataagaagat aaagggttcta cagatgtttt cttagcttcc ttttattgct atgaagtga 702

<210> 10
<211> 180
<212> PRT
<213> Mus musculus

<400> 10
Met Phe Gly Phe Phe Cys Ser Leu Val Ser Ser Leu Ser Arg Trp Phe
1 5 10 15
Leu Trp Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Asn Leu
20 25 30
Pro Leu Gln Val Lys Phe Ala Met Leu Glu Leu His Ser Phe Lys Cys
35 40 45
Pro Ala Gly Glu Tyr Trp Ser Lys Asp Val Cys Cys Lys Asn Cys Ser
50 55 60
Ala Gly Thr Phe Val Lys Ala Pro Cys Glu Ile Pro His Thr Gln Gly
65 70 75 80
Gln Cys Glu Lys Cys His Pro Gly Thr Phe Thr Glu Lys Asp Asn Tyr
85 90 95
Leu Asp Ala Cys Ile Leu Cys Ser Thr Cys Asp Lys Asp Gln Glu Met
100 105 110
Val Ala Asp Cys Ser Ala Thr Ser Asp Arg Lys Cys Gln Cys Arg Thr
115 120 125
Gly Leu Tyr Tyr Tyr Asp Pro Lys Phe Pro Glu Ser Cys Arg Pro Cys
130 135 140
Thr Lys Cys Pro Gln Gly Ile Pro Val Leu Gln Glu Cys Asn Ser Thr
145 150 155 160
Ala Asn Thr Val Cys Ser Ser Ser Val Ser Arg Arg Ser Ala Ser Val
165 170 175
Ala Trp Pro Ile
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<210> 11
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<220>
<223> Primer 2038-41

<400> 11
catactagtt ccaccatggtt tgggtttcttc tgcagcttgg t

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<210> 12
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<220>
<223> tmst2-Ig fusion protein

<400> 12
ttgtcgacat ttgaaacaga tgaactgcac aca 33

<210> 13
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion protein
consisting of Mus musculus sequences and
Immunoglobulin sequences

<220>
<221> CDS
<222> (1)..(1194)

<400> 13
atg ttt ggc ttc ttc tgc agc ttg gtg tcc agt ctg agt cgc tgg ttc 48
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1 5 10 15

ctt tgg cgg cgg ctg ctg ctg ctg ctg ctg ctg ctg ctg ctg aat ctg 96
Leu Trp Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Asn Leu
20 25 30

ccc ttg cag gta aaa ttt gct atg cta gaa tta cac tcc ttc aaa tgt 144
Pro Leu Gln Val Lys Phe Ala Met Leu Glu Leu His Ser Phe Lys Cys
35 40 45

ccc gct ggt gaa tac tgg tct aaa gac gtc tgt tgc aag aac tgt tct 192
Pro Ala Gly Glu Tyr Trp Ser Lys Asp Val Cys Cys Lys Asn Cys Ser
50 55 60

gca ggt aca ttt gtc aag gcg ccc tgc gaa atc ccc cat act caa gga 240
Ala Gly Thr Phe Val Lys Ala Pro Cys Glu Ile Pro His Thr Gln Gly
65 70 75 80

caa tgt gag aag tgt cac cca gga aca ttc aca gag aaa gat aat tac 288
Gln Cys Glu Lys Cys His Pro Gly Thr Phe Thr Glu Lys Asp Asn Tyr
85 90 95

ctg gat gct tgt ata ctt tgc tcc acc tgt gat aaa gat cag gaa atg 336
Leu Asp Ala Cys Ile Leu Cys Ser Thr Cys Asp Lys Asp Gln Glu Met
100 105 110

gtg gcc gac tgc tca gcc acc agt gac cgg aaa tgc cag tgc cga aca 384
Val Ala Asp Cys Ser Ala Thr Ser Asp Arg Lys Cys Gln Cys Arg Thr
115 120 125

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ggt ctt tac tac tat gac cca aaa ttt cca gaa tcg tgc cgc cca tgt	432
Gly Leu Tyr Tyr Tyr Asp Pro Lys Phe Pro Glu Ser Cys Arg Pro Cys	
130 135 140	
acc aag tgt ccc caa gga atc cct gtc ctc cag gaa tgc aac tcc aca	480
Thr Lys Cys Pro Gln Gly Ile Pro Val Leu Gln Glu Cys Asn Ser Thr	
145 150 155 160	
gct aac act gtg tgc agt tca tct gtt tca aat gtc gac act cac aca	528
Ala Asn Thr Val Cys Ser Ser Ser Val Ser Asn Val Asp Thr His Thr	
165 170 175	
tgc cca cag tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc	576
Cys Pro Pro Cys Pro Ala Pro Glu Leu Gly Gly Pro Ser Val Phe	
180 185 190	
ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct	624
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro	
195 200 205	
gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc	672
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val	
210 215 220	
aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca	720
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr	
225 230 235 240	
aag ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc	768
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val	
245 250 255	
ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc	816
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys	
260 265 270	
aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc	864
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser	
275 280 285	
aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca	912
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro	
290 295 300	
tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc	960
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val	
305 310 315 320	
aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg	1008
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly	
325 330 335	
cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac	1056
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp	
340 345 350	
ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg	1104
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp	
355 360 365	

cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac 1152
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
370 375 380

aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tgataa 1200
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
385 390 395

<210> 14

<211> 398

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion protein
consisting of Mus musculus sequences and
Immunoglobulin sequences

<400> 14

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Leu Trp Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Asn Leu
20 25 30

Pro Leu Gln Val Lys Phe Ala Met Leu Glu Leu His Ser Phe Lys Cys
35 40 45

Pro Ala Gly Glu Tyr Trp Ser Lys Asp Val Cys Cys Lys Asn Cys Ser
50 55 60

Ala Gly Thr Phe Val Lys Ala Pro Cys Glu Ile Pro His Thr Gln Gly
65 70 75 80

Gln Cys Glu Lys Cys His Pro Gly Thr Phe Thr Glu Lys Asp Asn Tyr
85 90 95

Leu Asp Ala Cys Ile Leu Cys Ser Thr Cys Asp Lys Asp Gln Glu Met
100 105 110

Val Ala Asp Cys Ser Ala Thr Ser Asp Arg Lys Cys Gln Cys Arg Thr
115 120 125

Gly Leu Tyr Tyr Tyr Asp Pro Lys Phe Pro Glu Ser Cys Arg Pro Cys
130 135 140

Thr Lys Cys Pro Gln Gly Ile Pro Val Leu Gln Glu Cys Asn Ser Thr
145 150 155 160

Ala Asn Thr Val Cys Ser Ser Ser Val Ser Asn Val Asp Thr His Thr
165 170 175

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
180 185 190

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
195 200 205

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
210 215 220

Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr
225					230					235					240
Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val
			245						250					255	
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys
		260						265					270		
Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser
		275					280						285		
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro
	290					295					300				
Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val
305					310					315					320
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly
				325					330					335	
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp
			340					345					350		
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp
		355					360					365			
Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His
	370					375					380				

Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys
385					390					395			

<210> 15

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Systhetic peptide

<400> 15

Tyr	Gly	Arg	Lys	Lys	Arg	Arg	Gln	Arg	Arg	Arg
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